



results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1050528130-021341-18840

Query=

(533 letters)

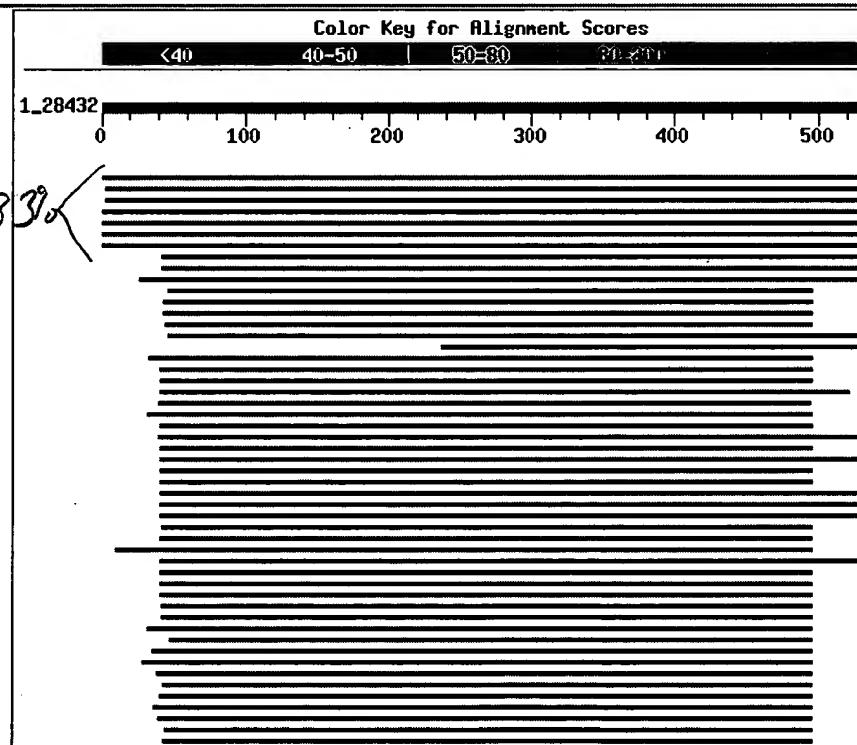
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
1,421,989 sequences; 457,202,972 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Taxonomy reports

Distribution of 110 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

(bits) Value

gi 5771354 dbj BAA83501.1	Sucrose Transporter [Zea mays]	838	0.0
gi 9624451 gb AAF90181.1 AF280050_1	sucrose transporter [Or...]	758	0.0
gi 7489560 pir T02982	probable sucrose transport protein -...	753	0.0
gi 20152871 gb AAM13408.1 AF408842_1	sucrose transporter SU...	752	0.0
gi 7024415 emb CAB75882.1	sucrose transporter 1 [Hordeum v...	751	0.0
gi 20152873 gb AAM13409.1 AF408843_1	sucrose transporter SU...	749	0.0
gi 19548165 gb AAL90455.1 AF408845_1	sucrose transporter SU...	747	0.0
gi 16152148 gb AAL14982.1 AF419298_1	sucrose transporter [O...	586	e-166
gi 15718401 dbj BAB68368.1	sucrose transporter [Oryza sati...	586	e-166
gi 21063927 gb AAM29153.1	sucrose transporter 2 [Citrus si...	526	e-148
gi 29467454 dbj BAC67164.1	sucrose transporter [Oryza sati...	526	e-148
gi 10119908 gb AAG12987.1 AF166498_1	sucrose transporter-li...	525	e-148
gi 15227049 ref NP_178389.1	putative sucrose/H ⁺ symporter;...	523	e-147
gi 6434831 gb AAF08330.1 AF021809_1	putative sucrose transp...	517	e-145
gi 29467456 dbj BAC67165.1	sucrose transporter [Oryza sati...	502	e-141
gi 19071641 gb AAL84308.1 AC073556_25	sucrose transporter, ...	416	e-115
gi 542020 pir S43142	sucrose transport protein - castor be...	385	e-105
gi 4091891 gb AAC99332.1	sucrose transporter [Apium graveo...	369	e-101
gi 15217601 ref NP_177333.1	sucrose transport protein SUC1...	369	e-101
gi 5566434 gb AAD45390.1 AF167415_1	sucrose transporter SUT...	367	e-100
gi 28172870 emb CAD61275.1	sucrose transporter 4 protein [...]	365	1e-99
gi 5882292 gb AAD55269.1 AF182445_1	sucrose transporter [Vi...	364	2e-99
gi 15239949 ref NP_196235.1	sucrose transporter protein; p...	364	2e-99
gi 1086253 pir S38657	sucrose transport protein ptp1 - com...	364	2e-99
gi 18091779 gb AAL58071.1	sucrose transporter SUC1 [Brassi...	364	2e-99
gi 5230818 gb AAD41024.1	sucrose transport protein SUT1 [P...	363	4e-99
gi 15219938 ref NP_173685.1	putative sucrose transport pro...	363	4e-99
gi 481131 pir S38196	sucrose transport protein SUC2 - Arab...	363	4e-99
gi 7488866 pir T12198	sucrose transport protein - fava bea...	363	5e-99
gi 7488936 pir T14340	sucrose-proton transport protein - c...	363	6e-99
gi 7488935 pir T14339	sucrose-proton transport protein - c...	362	6e-99
gi 6705993 dbj BAA89458.1	sucrose transporter protein [Dau...	362	7e-99
gi 15219686 ref NP_176830.1	sucrose-proton symporter, puta...	362	9e-99
gi 15217602 ref NP_177334.1	putative sucrose transport pro...	362	1e-98
gi 12057172 emb CAC19851.1	sucrose trasporter [Arabidopsis...	361	1e-98
gi 20147213 gb AAM10322.1	At1g22710/T22J18_12 [Arabidopsis...	361	2e-98
gi 12038843 emb CAC19689.1	sucrose/proton symporter [Daucu...	361	2e-98
gi 18091781 gb AAL58072.1	sucrose transporter SUC2 [Brassi...	359	5e-98
gi 9957218 gb AAG09270.1 AF176950_1	sucrose transporter [Ly...	359	6e-98
gi 10998390 gb AAG25923.1	sucrose transporter SUT4 [Solanu...	358	9e-98
gi 6434829 gb AAF08329.1 AF021808_1	putative sucrose transp...	358	2e-97
gi 9957053 gb AAG09191.1 AF175321_1	sucrose transporter SUT...	356	6e-97
gi 15225986 ref NP_179074.1	putative sucrose-proton sympor...	355	8e-97
gi 15218362 ref NP_172467.1	putative sucrose/H ⁺ symporter;...	355	1e-96
gi 542087 pir JQ2389	sucrose transport protein - potato >gi ...	355	1e-96
gi 7649151 gb AAF65765.1 AF242307_1	sucrose transport prote...	352	9e-96
gi 6434833 gb AAF08331.1 AF021810_1	putative sucrose transp...	350	3e-95
gi 15239921 ref NP_199174.1	sucrose transporter protein; p...	350	3e-95
gi 549000 sp Q03411 STP SPIOL	Sucrose transport protein (Su...	348	1e-94
gi 1076644 pir S48789	sucrose transport protein - common t...	347	2e-94
gi 5823000 gb AAD53000.1 U64967_1	sucrose-proton symporter ...	346	6e-94
gi 17447420 gb AAF04295.2 AF191025_1	sucrose transporter 1 ...	345	8e-94
gi 6120115 gb AAF04294.1 AF191024_1	sucrose transporter 1 [...]	345	1e-93
gi 21063921 gb AAM29150.1	citrus sucrose transporter 1 [Ci...	345	1e-93
gi 1086250 pir S52377	sucrose transport protein SUC1 - com...	342	1e-92
gi 1076257 pir S51114	sucrose-proton symporter - beet >gi ...	340	5e-92
gi 7024413 emb CAB75881.1	sucrose transporter 2 [Hordeum v...	338	1e-91
gi 29467452 dbj BAC67163.1	sucrose transporter [Oryza sati...	337	4e-91
gi 15217323 gb AAK92667.1 AC090487_9	Putative sucrose trans...	318	2e-85
gi 25344709 pir A86234	hypothetical protein [imported] - A...	315	1e-84
gi 575299 emb CAA57726.1	sucrose transporter [Lycopersicon...	296	7e-79
gi 1076602 pir S48788	sucrose transport protein - tomato (...)	295	1e-78
gi 2980887 emb CAA12256.1	Sucrose carrier [Ricinus communis]	295	1e-78



Protein

PubMed Nucleotide Protein Genome Structure PMC Taxonomy MIM Books

Search **Protein** for

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Display default Show: 20 Send to File Get Subsequence

□1: BAA83501. Sucrose Transporter...[gi:5771354]

BLink, Domains, Links

LOCUS BAA83501 521 aa linear PLN 26-AUG-1999
 DEFINITION Sucrose Transporter [Zea mays].
 ACCESSION BAA83501
 VERSION BAA83501.1 GI:5771354
 DBSOURCE accession AB008464.1
 KEYWORDS
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (sites)
 AUTHORS Aoki,N., Hirose,T., Takahashi,S., Ono,K., Ishimaru,K. and Ohsugi,R.
 TITLE Molecular cloning and expression analysis of a gene for a sucrose
 transporter in maize (Zea mays L.)
 JOURNAL Plant Cell Physiol. (1999) In press
 REFERENCE 2 (residues 1 to 521)
 AUTHORS Aoki,N.
 TITLE Direct Submission
 JOURNAL Submitted (24-OCT-1997) Naohiro Aoki, Japan International Research
 Center for Agricultural Sciences, Biological Resources Division;
 1-2 Ohwashi, Tsukuba, Ibaraki 305, Japan
 (E-mail:naoki@ss.jircas.affrc.go.jp, Tel:81-0298-38-6305,
 Fax:81-0298-38-6650)
 FEATURES Location/Qualifiers
 source 1..521
 /organism="Zea mays"
 /db_xref="taxon:4577"
Protein 1..521
 /product="Sucrose Transporter"
CDS 1..521
 /gene="ZmSUT1"
 /coded_by="AB008464.1:168..1733"
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 1 margdgelel svgvrgtgg aaaaaadhva pislgirlila gmvaggvgqyg walqlslltp
 61 yvqtglsha ltsfmwlcp iaglvqvplv glysdrctar wgrrrpfil gcmliclavi
 121 vvgfssdiga algdtkehcs lyhgprwhaa ivyvlgfll dfsnntvqgp arammadlcg
 181 hhgpsaansi fcswmalgni lgyssgstnn whkwfpflnt nacceacanl kgafolvavvf
 241 lvmcltvtf fanevpypyrgn qnlptkange vetepsgpla vlkgfknlpt gmpsvllvtg
 301 ltwlswfpfi lydtdwmgre iyhgdpkgsn aqisafdegv rvgsfgllln sivlgfssfl
 361 iepmcrkvgp rvvwvtsnm vcvamaatal isfwslkdhy gyvqdaitas tsikavclvl
 421 faflgvplai lysvpfavta qlaatkgggg glctgvlnis ivipqviial gagpwdalfg
 481 kgnipafgva sgfaliggvv gvfllpkisk rqfravsagg h
 //

gi 4960089 gb AAD34610.1 AF149981_1	sucrose transporter-like protein	294	2e-78
gi 16930709 gb AAL32020.1	sucrose transporter [Vitis vinifera L.]	277	2e-73
gi 13186184 emb CAC33492.1	sucrose carrier [Ricinus communis L.]	269	8e-71
gi 14161680 gb AAK54856.1	sucrose transporter [Oryza sativa L.]	241	2e-62
gi 14161682 gb AAK54857.1	sucrose transporter [Oryza sativa L.]	239	6e-62
gi 27227722 emb CAD29832.1	sucrose transporter [Viscum album L.]	222	1e-56
gi 17402525 dbj BAB78696.1	sucrose transporter [Nicotiana tabacum L.]	220	4e-56
gi 28830172 gb AAO52628.1	similar to Arabidopsis thaliana sucrose transporter	211	3e-53
gi 5640023 gb AAD45932.1 AF168771_1	sucrose transport protein	211	3e-53
gi 28371870 gb AAO38059.1	sucrose transporter SUC1 [Brassica napus L.]	177	3e-43
gi 28143940 gb AAO26335.1	putative sucrose transporter [Brassica napus L.]	159	2e-37
gi 27447671 gb AAO13696.1	sucrose transporter [Lycopersicon esculentum Mill.]	137	4e-31
gi 26522780 dbj BAC44864.1	hypothetical protein [Glycine max L.]	110	5e-23
gi 11596257 gb AAG38546.1 AF309805_11	putative sucrose carrier	102	2e-20
gi 28917846 gb EAA27533.1	hypothetical protein [Neurospora crassa] (partial)	100	7e-20
gi 19115299 ref NP_594387.1	putative sucrose carrier [Schinia sp.]	99	1e-19
gi 21426811 ref NP_653348.1	proton-associated sugar transporter	99	2e-19
gi 16716355 ref NP_444307.1	membrane associated transporter	98	3e-19
gi 21293355 gb EAA05500.1	agCP10413 [Anopheles gambiae strain 2Lc]	98	4e-19
gi 17369709 sp Q9UMX9 MATP HUMAN	Membrane-associated transmembrane protein	97	5e-19
gi 26354753 dbj BAC41003.1	unnamed protein product [Mus musculus]	97	5e-19
gi 28872809 ref NP_057264.2	membrane-associated transporter	97	5e-19
gi 15004313 gb AAK77024.1 AF332510_1	membrane-associated transporter	97	6e-19
gi 27688281 ref XP_226834.1	similar to membrane associated transporter	97	7e-19
gi 27719225 ref XP_235397.1	similar to KIAA1126 protein [Homo sapiens]	95	3e-18
gi 13097810 gb AAH03597.1 AAH03597	Similar to AIM-1 protein	92	2e-17
gi 27948583 gb AAO25647.1	membrane-associated transporter	92	2e-17
gi 21244213 ref NP_643795.1	sugar transporter [Xanthomonas campestris subsp. campestris]	92	2e-17
gi 24661424 ref NP_648292.1	CG4484-PA [Drosophila melanogaster]	91	4e-17
gi 21232786 ref NP_638703.1	sugar transporter [Xanthomonas campestris subsp. campestris]	89	1e-16
gi 6651341 gb AAF22281.1 AF167417_1	putative sucrose transporter	88	4e-16
gi 22122421 ref NP_666089.1	hypothetical protein MGC32471	85	3e-15
gi 27712020 ref XP_222629.1	similar to hypothetical protein	84	4e-15
gi 14916437 ref NP_149093.1	protein [Homo sapiens]	83	1e-14
gi 21294249 gb EAA06394.1	ebiP8133 [Anopheles gambiae strain 2Lc]	81	3e-14
gi 13874497 dbj BAB46871.1	hypothetical protein [Macaca fasciata]	81	4e-14
gi 6473156 dbj BAA87101.1	Hypothetical protein [Schizosaccharomyces pombe]	79	1e-13

Alignments Get selected sequences Select all Deselect all

>gi | 5771354 | dbj | BAA83501.1 | Sucrose Transporter [Zea mays]
Length = 521

Score = 838 bits (2166), Expect = 0.0
Identities = 447/538 (83%), Positives = 461/538 (85%), Gaps = 22/538 (4%)

Query: 1 MARGDGGQLAELSAGVRGAAA-----VVDHVAPISLGRLILAGMVAPISLGRLILAGMVA 55
MARDG ELS GVRG DHVAPISLG RLILAGMVA
Sbjct: 1 MARGDGE--LELSVGVRGTGGAAAAAADHVAPISLG-----RLILAGMVA 44

Query: 56 GGVQYGWALQLSLLTPYVQTLGLSHALTSMWLCLGPIAGLVVQPLVGLYSDRCTSRWGRR 115
GGVQYGWALQLSLLTPYVQTLGLSHALTSMWLCLGPIAGLVVQPLVGLYSDRCT+RWGRR
Sbjct: 45 GGVQYGWALQLSLLTPYVQTLGLSHALTSMWLCLGPIAGLVVQPLVGLYSDRCTARWGRR 104

Query: 116 RPFILTGCMLICVAVIVVGSSDGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLDFSN 175
RPFIL GCMLIC+AVIVVGSSDGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLDFSN
Sbjct: 105 RPFILIGCMLICLAVIVVGSSDGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLDFSN 164

Query: 176 NTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPLKTSACC 235

Sbjct: 165 NTVQGPARAMMADLC HHGPAANSIFCSWMALGNILGYSSGSTNNWHKWFPL T+ACC 224

Query: 236 EACANLKGXXXXXXXXXXXXXXXXXXXXFAKEVPYRANEVLPTTKAGGEVETEPTGPLAVLK 295
EACANLKG FA EVPYR N+NLP TKA GEVETEP+GPLAVLK
Sbjct: 225 EACANLKGAFLVAVVFLVMCLTVTLFFANEVPYRGNQNL -TKANGEVETEPTSGPLAVLK 283

Query: 296 GFKDLPPGMPSPVLLVTAITWLSWFPFILYD TDWMGREIYHGDPKGNSAQISAFNEGVRVG 355
GFK+LP GMPSVLLVT +TWLSWFPFILYD TDWMGREIYHGDPKGNSAQISAF+EGVRVG
Sbjct: 284 GFKNLPTGMPSPVLLVTGLTWLSWFPFILYD TDWMGREIYHGDPKGNSAOISAFDEGVRVG 343

Query: 356 AFGLLLNSVI LGFSSFLIEPMCRKVGP RVVWTSNFMCVAMAATALISFWSLRDYHGVV 415
+FGLLLNS++LGFSSFLIEPMCRKVGP RVVWTSNFMCVAMAATALISFWSL+DYHGVV
Sbjct: 344 SEGLLJNSVI LGFSESSLIEPMCRKVGP RVVWTSNFMCVAMAATALISFWSLKD YHGVV 403

Query: 416 QDAITANASIKAVCLVLFAGLGVPLAILYSPFAVTAQLAATRGQQQLCTGVLNISIVI 475
 QDAITA+ SIKAVCLVLFAGLGVPLAILYSPFAVTAQLAAT+GGGQQLCTGVLNISIVI
Sbjct: 404 QDAITASTSIKAVCLVLFAGLGVPLAILYSPFAVTAQLAATKGCCCGQLCTGVLNISIVI 463

Query: 476 PQVIIALGAGPWDALFGKGNIPXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533
PQVIIALGAGPWDALFGKGNIP PKISKRQFRAVSAGGH
Subject: 464 PQVIIALGAGPWDALFGKGNIPAEQVAVSGENLICCVYCVELLPKISKRQFRAVSAGGH 521

>gi|9624451|gb|AAF90181.1|AF280050_1 sucrose transporter [Oryza sativa (indica c
Length = 538]

Score = 758 bits (1958), Expect = 0.0
Identities = 399/529 (75%), Positives = 432/529 (81%), Gaps = 4/529 (0%)

Query: 4 GDGGQLAELSAGVRGAAAVVDHVAPISLGLRLILAGMVAPISLGLRLILAGMVAGGVQYQWA 63
G GG ELS G APISLGLRLIL+GMVAGGVQYQWA
Sbjct: 12 GGGGGCIELS---VGVGGGGGARGGGGCAAAAVETAAPISLGLRLILAGMVAGGVQYQWA 68

Query: 64 LQLSLLTPVQTLGLSHALTSMWLCGPIAGL VVQPLVGLYSDRCTSRWGRRRP+FILTGC 123
LQLSLLTPVQTLGLSHALTSMWLCGPIAG+VVQP VGLYSDRCTS+WGRRRP+ILTGC
Sbjct: 68 LQLSLLTPVQTLGLSHALTSEMWLCCGPIAGLVVQPLVGLYSDRCTSKWGRRRP+FILTGC 128

Query: 124 MLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLDFSNNTVQGP 183
+LIC+AV+V+GFS+DIG A+GDTKE CS+YHG RWHAIAIVYVLGFWLDFSNNTVQGP
Sbjct: 128 VIICLAVVIVGESADIGAAMGDTKEPCCSYIICGPWHAAIVYVLGFWLDFSNNTVQGP 182

Query: 184 AMMADLCDHHGPAANSIFCSWMALGNILGYSSGSTNNWHKWFPLKTSACCEACANLKG 243
A+MADL HGP ANSIFCSWMAGNILGYSSGSTNNWHKWFPLKTSACCEACANLKG
Subject: 182 ALMADLCDHGCTANSIFCSWMALGNILGYSSGSTNNWHKWFPLKTSACCEACANLKG 243

Query: 244 XXXXXXXXXXXXXXXX!FAKEVPYRANENLPTTKAGGEVETEPTGPLAVLKGFKDLPPG 303
 !FAKEVP++ N LP TK+ E E TGPLAVLKGF++LP G

Query: 304 MPSVLLVTAITWLSWFPFILYDTDWMGREIYHGDPKGSNAQISAFNEGVRVGAFGLLLNS 363
MPSVLT+VT +TWLSWFPFILYDTDWMGREIYHGDPKG++ QI AFN+GVR GAFLGLLNS

Query: 364 VILGFSSFLIEPMCRKVGPVVWTSNFVCVAMAATALISFWSLRDYHGYVQDAITANA 423
+ +LGFSSFLIEPMCRKVGPVVWTSNF+VC+AMAATALISFWSL+D+HG VQ AITA+

Query: 424 SIKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVIIALG 483
SIKAVCLVLFAFLGVPLA+LYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQV+IALG

Query: 484 AGPWDALFGKGNIXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGG 532

Subjct: 488 AGPWDELFGKGNIPAFGLASGFALIGGVAGIFLLPKISKRQFRSVSMGG 536

>gi|7489560|pir||T02982 probable sucrose transport protein - rice
 gi|2723471|dbj|BAA24071.1| sucrose transporter [Oryza sativa (japonica cultivar-g
 Length = 537

Score = 753 bits (1944), Expect = 0.0
 Identities = 397/529 (75%), Positives = 430/529 (81%), Gaps = 5/529 (0%)

Query: 4 GDGGQLAELSAGVRGAAAVDHVAPISLGLRLILAGMVAPISLGLRLILAGMVAGGVQYQWA 63
 G GG ELS APISLGLRLIL+GMVAGGVQYQWA
 Sbjct: 12 GGGGGGLELS----VGVGGGGARGGGGEAAAATAPISLGLRLILSGMVAGGVQYQWA 67

Query: 64 LQLSLLTPYVQTLGLSHALTSFMWLCPPIAGLVVQPLVGLYSDRCTS RWGRRRPFILTGC 123
 LQLSLLTPYVQTLGLSHALTSFMWLCPPIAG+VVQP VGLYSDRCTS+WGRRRP+ILTGC
 Sbjct: 68 LQLSLLTPYVQTLGLSHALTSFMWLCPPIAGMVVQPCVGLYSDRCTS KWGRRRPYILTGC 127

Query: 124 MLICVAIVVGFSSDIGAALGDTKEHCSLYHGPRWHAIIIVYVLGFWLLDFSNNTVQGP 183
 +LIC+AV+V+GFS+DIG A+GDTKE CS+YHG RWHAIIIVYVLGFWLLDFSNNTVQGP
 Sbjct: 128 VLICLAVVVIGFSADIGYAMGDTKEDCSVYHGSRWHAIIIVYVLGFWLLDFSNNTVQGP 187

Query: 184 AMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTMNNWHKFPLKTSACCEACANLKG 243
 A+MADL HGP ANSIFCSWMA+GNILGYSSGSTMNNWHKFPLKTSACCEACANLKG
 Sbjct: 188 ALMADLSGRHGP GTANSIFCSWMAMGNILGYSSGSTMNNWHKFPLKTRACCEACANLKG 247

Query: 244 XXXXXXXXXXXXXXXXXIFAKEVPYRANE NLPTTKAGGEVETEPTGPLAVLKGFKDLPPG 303
 IFAKEVP++ N LP TK+ E E TGPLAVLKGF++LP G
 Sbjct: 248 AFLVAVIFLSLCLVITLIFAKEVPFKGNAALP-TKSNEPAEPGTGPLAVLKGFRLNPTG 306

Query: 304 MPSVLLVTAITWLSWFPFILYDTDWMGREIYHGDPKGNSAQISAFNEGVRVGA FGLLLNS 363
 MPSVLT+VT +TWLSWFPFILYDTDWMGREIYHGDPKG++ QI AFN+GVR GAFGLLLNS
 Sbjct: 307 MPSVLI VTGLTWLSWFPFILYDTDWMGREIYHGDPKGTDQIEAFNQGVRA GA FGLLLNS 366

Query: 364 VILGFSSFLIEPMCRKVGP RVVWVTSNFMVCVAMAATALISFWSLRDYHG YVQDAITANA 423
 ++LGFSSFLIEPMCRKVGP RVVWVTSNF+VC+AMAATALISFWSL+D+HG VQ AITA+
 Sbjct: 367 IVLG FSSFLIEPMCRKVGP RVVWVTSNFLVCIAMAATALISFWSLKDFHGTVQKA ITADK 426

Query: 424 SIKAVCLVLF AFLGVPLA ILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVII ALG 483
 SIKAVCLVLF AFLGVPLA+LYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQV+IALG
 Sbjct: 427 SIKAVCLVLF AFLGVPLA VLYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVVI ALG 486

Query: 484 AGPWDALFGKGNIPXXXXXXXXXXXXXPKISKRQFRAVSAGG 532
 AGPWD LFGKGNIP PKISKRQF +VS GG
 Sbjct: 487 AGPWDALFGKGNIPAFGLASGFALIGGVAGIFLLPKISKRQFWSVSMGG 535

>gi|20152871|gb|AAM13408.1|AF408842_1 sucrose transporter SUT1A [Triticum aestivum
 Length = 522

Score = 752 bits (1941), Expect = 0.0
 Identities = 398/533 (74%), Positives = 435/533 (81%), Gaps = 11/533 (2%)

Query: 1 MARGDGQLAELSAGVRGAAAVDHVAPISLGLRLILAGMVAPI SLGLRLILAGMVAGGVQY 60
 MARG G ELS GV G A ++ ISLGLRLILAGMVAGGVQY
 Sbjct: 1 MARGGGNGEVELSVG VGGGGAGAGGADAPAVD-----ISLGLRLILAGMVAGGVQY 50

Query: 61 GWALQLSLLTPYVQTLGLSHALTSFMWLCPPIAGLVVQPLVGLYSDRCTS RWGRRRPFIL 120
 GWALQLSLLTPYVQTLGLSHALTSFMWLCPPIAGLVVQP VGLYSD+CTSRWGRRRPFIL
 Sbjct: 51 GWALQLSLLTPYVQTLGLSHALTSFMWLCPPIAGLVVQPCVGLYSDKCTS RWGRRRPFIL 110

Query: 121 TGCMLICVAIVVGFSSDIGAALGDTKEHCSLYHGPRWHAIIIVYVLGFWLLDFSNNTVQG 180
 TGC+LIC+AV+VVGFS+DIGAALGD+KE CSLYHGPRWHAIIIVYVLGFWLLDFSNNTVQG
 Sbjct: 111 TGCILICIAVVVVGFSADIGAALGDSKEEC SLYHGPRWHAIIIVYVLGFWLLDFSNNTVQG 170

Query: 181 PARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTMNNWHKFPLKTSACCEACAN 240
 PARA+MADL HGPSAANSIFCSWMALGNILGYSSGSTMNNWHKFPL+T ACCEACAN
 Sbjct: 171 PARALMADLSAQHGPSAANSIFCSWMALGNILGYSSGSTMNNWHKFPLRTRACCEACAN 230

Query: 241 LKGXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLKGFKDL 300
 LKG IFAKE+PY+A LP TKA G+VE EPTGPLAV KGFK+L
 Sbjct: 231 LKGAFLVAVLFLAFCLVITVIFAKEIPYKAIAPLP-TKANGQVEVEPTGPLAVFKGFKNL 289

Query: 301 PPGMPSVLLVTAITWLSWFPFILYDTDWMGREIYHGDPKGSNAQISAFNEGVRVGAFGLL 360
 PPGMPSVLLVT +TWLSWFPFILYDTDWMGREIYHGDPKG+ + +AF GVR GAFGLL
 Sbjct: 290 PPGMPSVLLVTGLTWSWFPFILYDTDWMGREIYHGDPKGTDEANAFQAGVRAGAFGLL 349

Query: 361 LNSVILGFSSFLIEPMCRKVGPRVVWVTSNFMCVAMAATALISFWSLRDYHGYVQDAIT 420
 LNSV+LGFSSTLIEP+C++GPRVVWV+SNF+VC++MAA +IS+W+ +D HGY+Q AIT
 Sbjct: 350 LNSVVLGFSSFLIEPLCKRLGPRVVWVSSNFLVCLSMAAICIISWWATQDLHGYIQHAIT 409

Query: 421 ANASIKAVCLVLFALGVPPLAILEYSPFAVTAQLAAATRGQQGLCTGVLNISIVIPQVII 480
 A+ IK V L LFAFLG+PLAILEYSPFAVTAQLAA RGGGQGLCTGVLNII+IVIPQVII
 Sbjct: 410 ASKEIKIVS LAFLAFLGIPLAILEYSPFAVTAQLAAANRGQQGLCTGVLNIAIVIPQVII 469

Query: 481 ALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533
 A+GAGPWD LFGKGNIP PKIS+RQFRAVS GGH
 Sbjct: 470 AVGAGPWDALFGKGNIPAFGVASAFA LIGGIVGIFLLPKISRRQFRAVSGGGH 522

>gi|7024415|emb|CAB75882.1| sucrose transporter 1 [Hordeum vulgare subsp. vulgaris]
 Length = 523

Score = 751 bits (1939), Expect = 0.0
 Identities = 399/538 (74%), Positives = 434/538 (80%), Gaps = 20/538 (3%)

Query: 1 MARGDGQLAELS-----AGVRGAAVVDHVAPISLGRLILAGMVAPISLGRLILAGMVA 55
 MARG G ELS G A + ISLG RLILAGMVA
 Sbjct: 1 MARGGGNGEVELSVGVGGGGGAAPRAAEPAVQISLG-----RLILAGMVA 46

Query: 56 GGVQYGWALQLSLLTPVQTLGLSHALTSMWLCGPIAGLVVQPLVGLYSDRCTS RGRR 115
 GGVQYGWALQLSLLTPVQTLGLSHALTSMWLCGPIAGLVVQP VGLYSD+CTSRWGR 115
 Sbjct: 47 GGVQYGWALQLSLLTPVQTLGLSHALTSMWLCGPIAGLVVQPCVGLYSDKCTS RGRR 106

Query: 116 RPFI LTGCMLICVAVI VVGFS SDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFSN 175
 RPFI LTGC+LIC+AVI+VGFS+DIGAALGD+KE CSLYHGPRWHAAIVYVLGFWLLDFSN
 Sbjct: 107 RPFI LTGCVLICLAVI IVGFSADIGAALGDSKEEC SLYHGPRWHAAIVYVLGFWLLDFSN 166

Query: 176 NTVQGPARAMMADLCDHHG PSAANSIFCSW MALGNILGYSSG STNNWHKWFPLKTSACC 235
 NTVQGPARA+MADL HG PSAANSIFCSW MALGNILGYSSG STNNWHKWFPLKTSACC 235
 Sbjct: 167 NTVQGPARALMADLSAQHG PSAANSIFCSW MALGNILGYSSG STNNWHKWFPLKTSACC 226

Query: 236 EACANLKGXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLK 295
 EACANLKG IFAKEVPY+A LP TKA G+VE EPTGPLAV K
 Sbjct: 227 EACANLKGAFLVAVLFLSLALVITLIFAKEVPYKAIAPLP-TKANGQVEVEPTGPLAVFK 285

Query: 296 GFKDLPPGMPSVLLVTAITWLSWFPFILYDTDWMGREIYHGDPKGSNAQISAFNEGVRVG 355
 GFK+LPPGMPSVLLVT +TWLSWFPFILYDTDWMGREIYHGDPKG+ A+ +AF EGVR G
 Sbjct: 286 GFKNLPPGMPSVLLVTGLTWSWFPFILYDTDWMGREIYHGDPKGTPEANAFQEGVRAG 345

Query: 356 AFGLLLNSVILGFSSFLIEPMCRKVGPRVVWVTSNFMCVAMAATALISFWSLRDYHGYV 415
 AFGLLLNSV+LGFSSTLIEPMC+++GPRVVWV+SN +VC++MAA +IS+W+ +D HGY+
 Sbjct: 346 AFGLLLNSVVLGFSSFLIEPMCRKRLGPRVVWVSSNFLVCLSMAAICIISWWATQDLHGYI 405

Query: 416 QDAITANASIKAVCLVLFALGVPPLAILEYSPFAVTAQLAAATRGQQGLCTGVLNISIVI 475
 Q AITA+ IKAV L LFAFLG+PLAILEYSPFAVTAQLAA +GGGQGLCTGVLNII+IVI
 Sbjct: 406 QHAITASKEIKIVS LAFLAFLGIPLAILEYSPFAVTAQLAA NGGGQGLCTGVLNIAIVI 465

Query: 476 PQVIIALGAGPWDALFGKGNIPXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533
 PQVIIA+GAGPWD LFGKGNIP PKIS+RQFRAVS GGH
 Sbjct: 466 PQVIIAVGAGPWDALFGKGNIPAFGMASVFA LIGGVVGIFLLPKISRRQFRAVSGGGH 523

>gi|20152873|gb|AAM13409.1|AF408843_1 sucrose transporter SUT1B [Triticum aestivum]
 Length = 522

Score = 749 bits (1934), Expect = 0.0
 Identities = 398/533 (74%), Positives = 434/533 (81%), Gaps = 11/533 (2%)

Query: 1 MARGDGGQLAELSAAGVRGAAAVVDHVAPISLGRLILAGMVAPIISLGRLILAGMVAGGVQY 60
 MARG G ELS GV G A ++ ISLGRLILAGMVAGGVQY
 Sbjct: 1 MARGGGNGEVELSVGVGGGAGAGGADAPAVD-----ISLGRLILAGMVAGGVQY 50

Query: 61 GWALQLSLLTPVQTLGLSHALTSMWLCCPIAGLVVQPLVGLYSDRCTS RWGRPFIL 120
 GWALQLSLLTPVQTLGLSHALTSMWLCCPIAGLVVQP VGLYSD+CTSRWGRPFIL
 Sbjct: 51 GWALQLSLLTPVQTLGLSHALTSMWLCCPIAGLVVQPCVGLYSDKCTS RWGRPFIL 110

Query: 121 TGCMPLICVAVIVVGFS DIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFSNNTVQG 180
 TG +LIC+AV+VVGFS+DIGAALGD+KE CSLYHGPRWHAAIVYVLGFWLLDFSNNTVQG
 Sbjct: 111 TGYI LICI AVVVGFS ADIGAALGDSKEEC SLYHGPRWHAAIVYVLGFWLLDFSNNTVQG 170

Query: 181 PARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPLKTSACCEACAN 240
 PARA+MADL HGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPL+T ACCEACAN
 Sbjct: 171 PARALMADLSAQHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPLRTRACCEACAN 230

Query: 241 LKGXXXXXXXXXXXXX IFAKEVPYRANE NLPTTKAGGEVETEPTGPLAVLKGF KDL 300
 LKG IFAKE+PY+A LP TKA G+VE EPTGPLAV KGFK+L
 Sbjct: 231 LKG AFLVAVLFLAFCLVITVIFAKEIPYKAIAPLP-TKANGQVEVEPTGPLAVFKGF KNL 289

Query: 301 PPGMP SVLLVTAITWLSWFPFILYDTDWMGREIYHGDPKGNSAQISAFNEGVRVGAF GLL 360
 PPGMP SVLLVT +TWLSWFPFILYDTDWMGREIYHGDPKG+ +AF GVR GAF GLL
 Sbjct: 290 PPGMP SVLLVTGLTWSWFPFILYDTDWMGREIYHGDPKGT PDEANAFQAGVRAGAF GLL 349

Query: 361 LNSVILGFSSFLIEPMCRKVGPRVVWVTSNFMCVAMAATALISFWSLRDYHGYVQDAIT 420
 LNSV+LGFS SFLIEP+C++GPRVVWV+SNF+VC++MAA +IS+W+ +D HGY+Q AIT
 Sbjct: 350 LNSVVLGFSSFLIEPLCKRLGPRVVWVSSNFLVCLMSMAICIIISWWATQDMHGYIQHAIT 409

Query: 421 ANASIKAVCLVLF AFLGVPLA ILYSVPFAVTAQLAATRGQQGLCTGVLNISIVIPQVII 480
 A+ IK V L LFAFLGVPLA ILYSVPFAVTAQLA RGGQQGLCTGVLN+IVIPQVII
 Sbjct: 410 ASKEIKIVSLALFAFLGVPLA ILYSVPFAVTAQLAANRGQQGLCTGVLNIAIVIPQVII 469

Query: 481 ALGAGPWDALFGKGNIPXXXXXXXXXXXXXPKISKRQFR AVSAGGH 533
 A+GAGPWD LFGKGNIP PKIS+RQFR AVS GGH
 Sbjct: 470 AVGAGPWDALFGKGNIPAFGMASAFA LIGGIVGIFLLPKISRRQFR AVSGGGH 522

>gi|19548165|gb|AAL90455.1|AF408845 1 sucrose transporter SUT1D [Triticum aestivum
gi|20152875|gb|AAM13410.1|AF408844 1 sucrose transporter SUT1D [Triticum aestivum
 Length = 523

Score = 747 bits (1928), Expect = 0.0
 Identities = 397/538 (73%), Positives = 432/538 (80%), Gaps = 20/538 (3%)

Query: 1 MARGDGGQLAELSAAGVRGAAAVVDH----VAPISLGRLILAGMVAPIISLGRLILAGMVA 55
 MARG G ELS GV G ISLG RLILAGMVA
 Sbjct: 1 MARGGGNGEVELSVGVGGGAGAGGADAPAVD-----RLILAGMVA 46

Query: 56 GGVQYGWALQLSLLTPVQTLGLSHALTSMWLCCPIAGLVVQPLVGLYSDRCTS RWGR 115
 GGVQYGWALQLSLLTPVQTLGLSHALTSMWLCCPIAGLVVQP VGLYSD+CTSRWGR
 Sbjct: 47 GGVQYGWALQLSLLTPVQTLGLSHALTSMWLCCPIAGLVVQPCVGLYSDKCTS RWGR 106

Query: 116 RP FILTG CMLICVAVIVVGFS DIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFSN 175
 RP FILTG+C+AV+VVGFS+DIGAALGD+KE CSLYHGPRWHAAIVYVLGFWLLDFSN
 Sbjct: 107 RP FILTG CILICIAV VVGFS ADIGAALGDSKEEC SLYHGPRWHAAIVYVLGFWLLDFSN 166

Query: 176 NTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPLKTSACC 235
 NTVQGPARA+MADL HGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPL+T ACC
 Sbjct: 167 NTVQGPARALMADLSAQHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPLRTRACC 226

Query: 236 EACANLKGXXXXXXXXXXXXX IFAKEVPYRANE NLPTTKAGGEVETEPTGPLAVLK 295
 EACANLKG IFAKE+PY+A LP TKA G+VE EPTGPLAV K
 Sbjct: 227 EACANLKG AFLVAVLFLAFCLVITVIFAKEIPYKAIAPLP-TKANGQVEVEPTGPLAVFK 285

Query: 296 GFKDLPPGMPSVLLVTAITWLSWFPFILYDTDWMGREIYHGDPKGSNAQISAFNEGVRVG 355
 GFK+LPPGMPSVLLV +TWLSWFPFILYDTDWMGREIYHGDPKG+ + +AF GVR G
 Sbjct: 286 GFKNLPPGMPSVLLVTGLTWLSWFPFILYDTDWMGREIYHGDPKGTDEANAFQAGVRAG 345

Query: 356 AFGLLLNSVILGFSSFLIEPMCRKVGPRVVWTSNFMVCVAMAATALISFWSLRDYHGYV 415
 AFGLLLNSV+LGFSSFLIEP+C++GPRVVWV+SNF+VC++MAA +IS+W+ +D HGY+
 Sbjct: 346 AFGLLLNSVVLGFSSFLIEPLCKRLGPRVVWSSNFLVCLSMAAICIISWWATQDLHGYI 405

Query: 416 QDAITANASIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRGQQGLCTGVLNISIVI 475
 Q AITA+ IK V L LFAFLG+PLAILYSVPFAVTAQLA RGGGQQGLCTGVLN+IVI
 Sbjct: 406 QHAITASKEIKIVSLALFAFLGIPLAILYSVPFAVTAQLA AKRGQQGLCTGVLNIAIVI 465

Query: 476 PQVIIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533
 PQVIIA+GAGPWD LFGKGNIP PKIS+RQFRAVS GGH
 Sbjct: 466 PQVIIAVGAGPWDALFGKGNIPAFGMASAFA LIGGIVGIFLLPKISRRQFRAVSGGGH 523

>gi|16152148|gb|AAL14982.1|AF419298 1 sucrose transporter [Oryza sativa (indica
 Length = 506

Score = 586 bits (1511), Expect = e-166
 Identities = 330/494 (66%), Positives = 375/494 (75%), Gaps = 11/494 (2%)

Query: 43 ISLGRLLILAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSMWLCGPIAGLIVQPLVG 102
 ISL L LA MVAGGVQYGWALQLSLLTPY+QTLG+ HALTS MWLCGPIAGL+VQP VG
 Sbjct: 21 ISLSGLFLACMVAGGVQYGWALQLSLLTPYIQTGLGIPHALTSVMWLCGPIAGLIVQPCVG 80

Query: 103 LYSDRCTSRWGRRRPFILTGCMLICVAVIVVGFS SDIGAALGDTKEHCSLYHGPRWHAAI 162
 LYSD+CTS GRRRPFILTGC++IC++VIV+GFSSDIG ALGD E C +Y GPR+HAA
 Sbjct: 81 LYSDKCTSSLGRRRPFILTGCIIICISVIVIGFSS DIGYALGDATEDCKVYRGPRYHAA 140

Query: 163 VVVLGFWLLDFSNNTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNW 222
 ++LGFWLLDFSNNTVQGPARA+MADL HGPSAAN+IFCSWMALGNILGYSSGSTN+W
 Sbjct: 141 AFILGFWLLDFSNNTVQGPARALMADLSGRHGPSAANAIFCSWMALGNILGYSSGSTNDW 200

Query: 223 HKWFPFLKTSACCEACANLKXXXXXXXXXXXXXIFAKEVPYRANE NLPTTKAGGE 282
 HKWFPFL T ACCEACANLK +FA+EV L A
 Sbjct: 201 HKWFPFLMTRACCEACANLKAFLVAVVFLGLSTAVTMFAREVA-----LDPVAAA 254

Query: 283 VETEPTGPLAVLKGFKDLPGMPSVLLVTAITWLSWFPFILYDTDWMGREIYHGDPKGSN 342
 E E +GPLAV KG K+LP GMPSVL+VT +TWLSWFPFIL+DTDWMGREIYHG P GS
 Sbjct: 255 NEGEASGPLAVFKGMKNLPVGMPSPVLI VTGLTWLSWFPFILFDTDW MGREIYHGRPDGSP 314

Query: 343 AQISAFNEGVRVGAFLNNSVILGFSSFLIEPMCRKVGPRVVWTSNFMVCVAMAATAL 402
 A+++AF EGVR GAFGLLLNS++LG SSFLIEPMCR+G R VVW S+ +VCVAMAA ++
 Sbjct: 315 AEVTAFAQEGVRQGAFLNNSIVLGISSFLIEPMCRLGARAVVVMSSAVVCVAMAAVSV 374

Query: 403 ISFWSLRDYHGYVQDAITANAS---IKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRG 459
 +S WSL D+ G VQDA A A ++A L LF FLG+P A+L SVPFAVTAQL A+RG
 Sbjct: 375 LSAWSLGDFGGSVQDAARAPAEEGGV RASALALFVFLGLPFAVLCSVPFAVTAQLTASRG 434

Query: 460 GGQGLCTGVLNISIVIPQVIIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXPK 519
 GGQGLCTGVLNISIV+PQ+ IALGAGPWD LFG+GNIP PK
 Sbjct: 435 GGQGLCTGVLNISIVV PQM AIALGAGPWD LFGEGNI PAFAMASVFAAAAAAGVVLLPK 494

Query: 520 ISKRQFRAVSAGGH 533
 +S R AGGH
 Sbjct: 495 VSVRSVSM--AGGH 506

>gi|15718401|dbj|BAB68368.1| sucrose transporter [Oryza sativa (japonica cultiva
 Length = 506

Score = 586 bits (1511), Expect = e-166
 Identities = 332/494 (67%), Positives = 376/494 (76%), Gaps = 11/494 (2%)

Query: 43 ISLGLRILAGMVAGGVQYGWALQLSLLTPVQTLGLSHALTSMWLCGPIAGLVVQPLVG 102
 ISL L LA MVAGGVQYGWALQLSLLTPVQTLG+ HALTS MWLCGPIAGL+VQP VG
 Sbjct: 21 ISLSGLFLACMVAGGVQYGWALQLSLLTPVQTLGIPHALTSVMWLCGPIAGLIVQPCVG 80

Query: 103 LYSDRCTSRWGRRRPFILTGCMLICVAVIVVGFSIDIAGAALGDTKEHCSLYHGPRWHAAI 162
 LYSD+CTS GRRRPFILTGC++IC++VIV+GFSSDIG ALGDT E C +Y GPR+HAA
 Sbjct: 81 LYSDKCTSSLGRRRPFILTGCIIICISVIVIGFSSDIGYALGDTTEDCKVYRGPRYHAAA 140

Query: 163 VYVLGFWLDFSNNTVQGPARAMMADLCDHHGSAANSIFCSWMALGNILGYSSGSTNNW 222
 ++LGFWLDFSNNTVQGPARA+MADL HGPSAAN+IFCSWMALGNILGYSSGSTN+W
 Sbjct: 141 AFILGFWLDFSNNTVQGPARALMADLSGRHGPSAANAIFCSWMALGNILGYSSGSTNDW 200

Query: 223 HKWFPFLKTSACCEACANLKGXXXXXXXXXXXXXIFAKEVPYRANEMLPTTKAGGE 282
 HKWFPFL T ACCEACANLK +FA+EV L A
 Sbjct: 201 HKWFPFLMTRACCEACANLKAFLVAVVFLGLSTAVTMVFAREVA-----LDPVAAAKR 254

Query: 283 VETEPTGPLAVLKGFKDLPPGMPSVLLVTAITWLSWFPFILYDTDWMGREIYHGDPKGSN 342
 E E +G LAV KG K+LP GMPSVL+VT +TWLSWFPFIL+DTDWMGREIYHG P GS
 Sbjct: 255 NEGEASGLLAVFKGMKNLPVGMPSVLIVTGLTWLSWFPFILFDTDWMGREIYHGRPDGSP 314

Query: 343 AQISAFNEGVRVGAFLGLLLNSVILGFSSFLIEPMCRKVGPRVVWVTSNFMCVAMAATAL 402
 A+++AF EGVR GAFLGLLLNS++LG SSFLIEPMCR++G R VWV S+ +VCVAMAA ++
 Sbjct: 315 AEVTAFQEGVRQGAFLGLLLNSIVLGISSFLIEPMCRLGARAVWVMSSAVVCVAMAAVSV 374

Query: 403 ISFWSLRDYHGYVQDAITANAS---IKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRG 459
 +S WSL D+ G VQDA A A ++A L LF FLG+P A+L SVPFAVTAQLAA+RG
 Sbjct: 375 LSAWSLGDFGGSVQDAARAPAEEGGVRASALALFVFLGLPFAVLCSVPAVTAQLAASRG 434

Query: 460 GGQGLCTGVLNISIVIPQVIIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXPK 519
 GGQGLCTGVLNISIV+PQ+ IALGAGPWD LFG+GNIP PK
 Sbjct: 435 GGQGLCTGVLNISIVVQPMIAIALGAGPWDelfGEGNIPAFAMASVFAAAAAAGVVLIPK 494

Query: 520 ISKRQFRAVSAGGH 533
 +S R AGGH
 Sbjct: 495 VSVRSVSM--AGGH 506

>gi|21063927|gb|AAM29153.1| sucrose transporter 2 [Citrus sinensis]
 Length = 607

Score = 526 bits (1356), Expect = e-148
 Identities = 286/559 (51%), Positives = 359/559 (64%), Gaps = 54/559 (9%)

Query: 27 APISLGRLILAGMVAPISLGRLILAGMVAGGVQYGWALQLSLLTPVQTLGLSHALTSM 86
 +PI G A SL L+L+ VA GVQ+GWALQLSLLTPY+QTLG+ HA +SF+
 Sbjct: 49 SPIPNGTNSFAVRPKQCSLITLVLSCVAAVGQFGWALQLSLLTPYIQTGLGIQHAFSSFI 108

Query: 87 WLCGPIAGLVVQPLVGLYSDRCTSRWGRRRPFILTGCMLICVAVIVVGFSIDIAGAALGDT 146
 WLCGPI GLVVQP VG++SD+CTS++GRRRPFIL GC++I VAVI++GFS+DIG LGDT
 Sbjct: 109 WLCGPIGLVVQPCVGIWSDKCTSKYGRRRPFILAGCLMISVAVIIIGFSADIGYILGDT 168

Query: 147 KEHCSLYHGPRWHAAIVYVLGFWLDFSNNTVQGPARAMMADLCDHHGSAANSIFCSWM 206
 KEHCS + G R AA V+V+GFWLDD +NNTVQGPARA++ADL ++AN+I CSWM
 Sbjct: 169 KEHCSKFRGTRTRAFFVFIGFWLDDLANNTVQGPARALLADLSGPQRNSANAILCSWM 228

Query: 207 ALGNILGYSSGSTNNWHKFPLKTSACCEACANLKGXXXXXXXXXXXXXIFAKEV 266
 A+GNILG+S+G++ +WH+WFPFL ACC AC NLK FA EV
 Sbjct: 229 AVGNILGFSAGASGSWHRWFPLTSRACCAACGNLKAFLVAVVFLCALVTIYFADEV 288

Query: 267 PYRANE-----NLPT--TKAGGEVET----- 285
 P N+ ++P G +VE+
 Sbjct: 289 PLTVNQPNHLTDsapLLDDPQRTAISKSKHDMPAAPNANGNKVESGHERDANLKHISKKA 348

Query: 286 -EPT----GPLAV---LKGFKDLPNGMPSVLLVTAITWLSWFPFILYDTDWMGREIYH 335
 +P GP AV L + LPP M VL+V A+TWLSWFPF L+DTDWMGRE+YH
 Sbjct: 349 EDPNGSFNDGPGAVLVNLLTSLRHLPPAMHVVLMALTWLSWPFFLFDTDWMGREYH 408

Query: 336 GDPKGSNAQISAFNEGVRVGAFLGLLLNSVILGFSSFLIEPMCRKVGPRVVWTSNFMVCV 395
 GDPKG++ ++ +++GVR GAFGLLLNSV+LG SSFLIEPMCR +G R+VW SNF+V
 Sbjct: 409 GDPKGNDHEVKFYDQGVREGAFGLLLNSVLGVSFLIEPMCRWIGSRLVWAISNFIVFA 468

Query: 396 AMAATALISFWSL-RDYHGYVQDAITANASIKAVCLVLFAGLGVPLAILYSVPFAVTAQL 454
 MA TA+IS S+ R+ ++ I AN +IK LV+F LG PLAI YSVPFA+T +L
 Sbjct: 469 CMATTAIISVISVRRNILEGIEHGIGANQAIIKVASLUVFTLLGFPLAITYSVPFAITGEL 528

Query: 455 AATRGGGQGLCTGVLMISIVIPQVIIALGAGPWDALFGKGNIPXXXXXXXXXXXXXX 514
 A GGGQGL GVLM++IVIPQ+I++LGAGPWDALFG GNIP
 Sbjct: 529 TADSGGGQGLAIGVLMIAIVIPQMIVSLGAGPWDALFGGGNIPAFGLASLSLAGGVVAT 588

Query: 515 XXXPKISKQRQFRAVSAGGH 533
 P +S F S+G H
 Sbjct: 589 LKLPHLSSNSF--TSSGFH 605

>gi|29467454|gb|BAC67164.1| sucrose transporter [Oryza sativa (japonica cultivar group)]
 Length = 595

Score = 526 bits (1355), Expect = e-148
 Identities = 267/499 (53%), Positives = 344/499 (68%), Gaps = 48/499 (9%)

Query: 47 RLILAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSMWLCGPIAGLVVQPLVGLYSD 106
 +L+LA MVA GVQ+GWALQLSLLTPY+QTLG+ HA+ SF+WLCGPI G VVQP VG++SD
 Sbjct: 61 KLVLMACMVAAGVQFGWALQLSLLTPYIQTGLGIDHAMASFIWLCPITGFVVQPCVGVWSD 120

Query: 107 RCTS RWGRRRPFILTGCMLICVAIVVGFS DIGAALGDTKEHCSLYHGPRWHAAIVYVL 166
 +C S++GRRRPFIL GC++IC AV ++GFS+D+G LGDT EHCS Y G R+ AAI++VL
 Sbjct: 121 KCRSKYGRRRPFILAGCLMICFAVTLIGFSADLGYILGDTTEHCSTYKGSRFRAAIIFVL 180

Query: 167 GFWL LD FSNN TVQGP ARAMM ADI LCD HH GPSAANSIFCSWM ALGN ILGYSSG STNN WHKWF 226
 GFW+LD +N+TVQGP ARADL + +AN+IFC+WMA+GN+LG+SSG++ NWHKF
 Sbjct: 181 GFWML DL AN HTVQGP AR ALLADL SGPDQC NSANA IFCTWMA VGNV LGFSS GASGN WHKWF 240

Query: 227 PFLK TSACCEACANLK GXXXXXXXXXXXXX IFAKEV PYR----- 269
 PFL T ACCEAC+NLK FA+E+P
 Sbjct: 241 PFLMTRACCEACSNLKA AFLV A VV FLLFCMSVTLYFAEEI PLEPTD A QRL SDSAP LLNGS 300

Query: 270 -----ANENLPTTKAGGE-VETEPTGPLAV---LKGFK 298
 AN N + + E VE GP AV L +
 Sbjct: 301 RDDNNASNEPRNGALPNGHTDGSNPANSNAEDNSNRENVEVFNDGPGAVLVNILTSMR 360

Query: 299 DLPPGMPSVLLVTAITWLSWFPFILYD TDWMGREIYHGDPKGSNAQISAFNEGVRVGA FG 358
 LPPGM SVLLV A+TWLSWFPF L+DTDWMGRE+YHGDP G+ ++ A++ GVR GA FG
 Sbjct: 361 HLPPGMYSVLLVMALTWLSWFPFFLFD TDWMGREVYHGDPGNL SERKAYDNGVREGA FG 420

Query: 359 LLLNSVILGFSSFLIEPMCRKVGPRVVWTSNFMVCVAMAATALISFWSLRDYHGYVQDA 418
 LLLNSV+LGF SFL++P+CR +G R+VW SNF V + M ATA++S+ S Y +
 Sbjct: 421 LLLNSVVLGF GSFLVDPLCRLMGARLV WAISNFTV FICMLATAILSWISFDLYSSKLHHI 480

Query: 419 ITANASIKAVCLVLFAGLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQV 478
 I AN ++K L++F+ LG+PL+I Y VP+VTA+L A G GQGL TGVLN++IV+PQ+
 Sbjct: 481 IGANKTVKNSALIVFSLLGLPLSITYGV PFSVTAELTAGTGSGQGLATGVLNLAIVVPQI 540

Query: 479 IIALGAGPWDALFGKGNIP 497
 +++LGAGPWDALFG GN+P
 Sbjct: 541 VVSLGAGPWDALFGGGNVP 559

>gi|10119908|gb|AAG12987.1|AF166498.1| sucrose transporter-like protein [Lycopersicon esculentum (tomato)]
 Length = 604

Score = 525 bits (1353), Expect = e-148
 Identities = 269/508 (52%), Positives = 336/508 (66%), Gaps = 54/508 (10%)

Query: 44 SLGRLILAGMVAGGVQYGWALQLSLLTPVQTLGLSHALTSMWLCGPIAGLVVQPLVGL 103
 SL L+L+ VA GVQ+GWALQLSLLTPY+QTLG+ HA +SF+WLCGPI GLVVQP VG+
 Sbjct: 62 SLLTLILSCTVAAGVQFGWALQLSLLTPYIQTGIEHAFSSFIWLCGPITGLVVQPCVGI 121

Query: 104 YSDRCTS RWGRRRP FILTGCM LIC VAVIVVG FSSD IGA ALG DT KEHCS LYHG PRWHAAIV 163
 +SD+C S++GRRRPFI G ++I +AVI++GFS+DIG LGDT KEHCS + G R AAIV
 Sbjct: 122 WSDKCHSKYGRRRPFIFIGAVMISIAVIIGFSADIGYLLGDTKEHCSTFKGTRSRAAIV 181

Query: 164 YVLGFWL DFSNNTV QGP ARAMM ADL C DHG PSA A NS IF CSW M ALGN ILGY SS G STNN WH 223
 +V+GFW+LD +NNTV QGP AR A+ADL + AN++FCSWMA+GNILG+S+G++ WH
 Sbjct: 182 FVVGFWM LD LAN NTV QGP ALLADLSGP DQR NTANA VFCSWMA VGNILGFSAGASGGWH 241

Query: 224 KWFPFLK TSACCEACANLKGXXXXXXXXXXXXX XIFAKEVP----- 267
 +WFPFL ACCE C NLK FA EVP
 Sbjct: 242 RWFPFLTNRACCEPCGNLKAAFLVAVVFLTLCTLVTLYFANEVPLSPKQYKRM SDSAPLL 301

Query: 268 -----YRAN-----ENLPTTKAGGEVETEPTGP 290
 YR + E P G P
 Sbjct: 302 DSPQNTGF DLSQS KRELQYRNSVANNESEM GHVADN SPK NEEQ RPDKD QGD SFAD SPG AV 361

Query: 291 LA-VLKGFKDLPPGMPSVLLVTAITWLSWFPFILYDTDWMGREIYHGDPKG SNAQISAFN 349
 L +L + LPP M SVL+V A+TWLSWFPF L+DTDWMGRE+YHGDPKG +++A+N
 Sbjct: 362 LVNLLTSLRHLPPAMHSVLIVMAL TWLSWFPFFLFDTDWMGREVYHGDPKG EADEVNAYN 421

Query: 350 EGVRVGA FGLLL NSVIL GFSS FLIEPM CRKV GP RVV WTSN FMVC VAMA ATALIS FW SLR 409
 +GVR GAFG LLL NSV+LG SSFLIEPMC+ +G R+VW SNF+V V MA TA+IS S+
 Sbjct: 422 QGVREGA FGLLL NSVVLGVSS FLIEPM CKWIG SRLV WA VSNF IVF VCM ACTAI ISV VSIS 481

Query: 410 DYHGYVQDA ITAN ASIK A VCL VLFA FLGV PL AILY SVP FAVTA QLA ATRGGG QGL CTG VL 469
 VQ I A S + LV+F+ LG+PLA+ YSVP F++TA+L A GGGQ GL GVL
 Sbjct: 482 ANTQGVQHVIGATRSTQIA ALVV FSLL GIPLA VTYSVP FSITA ELTAD AGGG QGLA IG VL 541

Query: 470 NISIVIPQ VII ALGAGP WD ALFG KGNIP 497
 N++IV+PQ+++LGAGP WD ALFG GNIP
 Sbjct: 542 NLAIV VPQM VV S LGAGP WD ALFG GGNIP 569

>gi|15227049|ref|NP_178389.1| putative sucrose/H+ symporter; protein id: At2g028
 thaliana]
 gi|25344715|pir||G84441 probable sucrose-proton symporter [imported] - Arabidopsi
 gi|3461813|gb|AAC32907.1| putative sucrose/H+ symporter [Arabidopsis thaliana]
 gi|8052190|emb|CAB92307.1| sucrose transporter [Arabidopsis thaliana]
 Length = 594

Score = 523 bits (1348), Expect = e-147
 Identities = 261/501 (52%), Positives = 336/501 (67%), Gaps = 47/501 (9%)

Query: 44 SLGRLILAGMVAGGVQYGWALQLSLLTPVQTLGLSHALTSMWLCGPIAGLVVQPLVGL 103
 SL L+L+ VA GVQ+GWALQLSLLTPY+QTLG+SHA +SF+WLCGPI GLVVQP VG+
 Sbjct: 59 SLVTLVL SCTVAAGVQFGWALQLSLLTPYIQTGISHAFSSFIWLCGPITGLVVQPFVGI 118

Query: 104 YSDRCTS RWGRRRP FILTGCM LIC VAVIVVG FSSD IGA ALG DT KEHCS LYHG PRWHAAIV 163
 +SD+CTS++GRRRPFI G +I +AVI++GFS+DIG LGD+KEHCS + G R AA+V
 Sbjct: 119 WSDKCTSKYGRRRPFILVGSFMISIAVIIGFSADIGYLLGDSKEHCSTFKGTRTRA AVV 178

Query: 164 YVLGFWL DFSNNTV QGP ARAMM ADL C DHG PSA A NS IF CSW M ALGN ILGY SS G STNN WH 223
 +GFWL LD +NNTV QGP AR A+ADL + AN+FC WMA+GNILG+S+G++ W
 Sbjct: 179 FIIGFWL LD LAN NTV QGP ALLADLSGP DQR NTANA VFCLWMAIGNILGFSAGASGKWQ 238

Query: 224 KWFPFLK TSACCEACANLKGXXXXXXXXXXXXX XIFAKEVPYRAN----- 271
 +WFPFL + ACC AC NLK FAKE+P+ +N
 Sbjct: 239 EWFPFLTSRACCAACGNLKAAFL LAVVFLTIC TLVTIYFAKEIPFTSNKPTRI QDSAPLL 298

Query: 272 -----ENLPTTKAGGEVETEPTGPLAV---LKG 296
 E ++ + ET GP +V L
 Sbjct: 299 DDLQSKGLEHSKLNNGTANGIKYERVERDTDEQFGNSENEHQDETYVDGPGSVLVNLLTS 358

Query: 297 FKDLPPGMPSVLLVTAITWLSWFPFILYDTDWMGREIYHGDPKGSNAQISAFNEGVRVGA 356
 + LPP M SVL+V A+TWLSWFPF L+DTDWMGRE+YHGDP G + + +++GVR GA

Sbjct: 359 LRHLPPAMHSVLIVMALTWLSWFPFFLFDTDWMGREVYHGDPTGDSLHMELYDQGVREGA 418

Query: 357 FGLLLNSVILGFSSFLIEPMCRKVGPVVWVTSNFMVCVAMAATALISFWSLRDYHGYVQ 416
 GLLLNSV+LG SSFLIEPMC++G RVVV SNF V MA TA+IS SL D ++

Sbjct: 419 LGLLLNSVVLGISSFLIEPMCQRMGARVVWALSNTVFACMAGTAVISLMSLSDDKNGIE 478

Query: 417 DAITANASIKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIP 476
 + N + + +++FA LG PLAI YSVPF+VTA++ A GGGQGL GVNL++IVIP

Sbjct: 479 YMRRGNETTRTAAVIVFALLGFPLAITYSVPFSVTAEVTADSGGGQGLAIGVNLAIVIP 538

Query: 477 QVIIALGAGPWDALFGKGNIP 497
 Q+I++LGAGPWD LFG GN+P

Sbjct: 539 QMIVSLGAGPWDQLFGGGNLP 559

>gi|6434831|gb|AAF08330.1|AF021809_1 putative sucrose transporter [Vitis vinifer
 Length = 612

Score = 517 bits (1331), Expect = e-145

Identities = 272/507 (53%), Positives = 340/507 (67%), Gaps = 54/507 (10%)

Query: 45 LGRLILAGMVAGGVQYGWALQLSLLTPYQTLGLSHALTSMWLCGPIAGLVVQPLVGLY 104
 L LIL+ M+A GVQ+GWALQLSLLTPY+QTLG+ HA +SF+WLCGPI GLVVQP VG++

Sbjct: 63 LRTLILSCMIAAGVQFGWALQLSLLTPYIQTGLIEHAFFSIWLCPITGLVVQPCVGIW 122

Query: 105 SDRCTSRWGRRRPFILTGCMLICVAVIVVGFSDDIGAALGDTKEHCSLYHGPRWHAAIVY 164
 SD+C+S++GRRRPFIL G ++I VAV ++GFS+DIG LGDT C + G R AAI++

Sbjct: 123 SDKCSSKYGRRRPFILAGSLMISVAVTIIGFSADIGYLLGDTNMDCRKFKGTRTWAAIIF 182

Query: 165 VLGFWLLDFSNNTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHK 224
 VLGFW+LD +NNTVQGPARA++ADL ++AN+I FCSWMA+GNILG+S+G++ +WH+

Sbjct: 183 VLGFWMULDLANNTVQGPARALLADLSGPQRNSANAI FCSWMAVGNILGFSAGASGHWHR 242

Query: 225 WFPFLKTSACCEACANLKGXXXXXXXXXXXXXIFAKEVP----- 267
 WFPFL ACCEAC NLK FA+EVP

Sbjct: 243 WFPFLNKACCEACGNLKAAFLIAVVFLTLCTLVTLYFAEEVPLMAYQPHHLSDSAPLLD 302

Query: 268 -----YRANENLP--TTKAGGEVETEPTGPLAV-- 293
 Y N+N T + E+ GP AV

Sbjct: 303 NPQQIGFDNSKS金陵MSAVDNATGNNPESSEYINKNAHLPIVQEQQNESFSDGPGAVLV 362

Query: 294 --LKGFKDLPNGMPSVLLVTAITWLSWFPFILYDTDWMGREIYHGDPKGSNAQISAFNEG 351
 L + LPP M SVLLV A++WLSWFPF L+DTDWMGRE+YHGDPKG + + A++ G

Sbjct: 363 NLLTSLRHLPPAMHSVLLVMALSWLSWFPFFLFDTDWMGREVYHGDPKGDESAVKAYDAG 422

Query: 352 VRVGAFLLLNSVILGFSSFLIEPMCRKVGPVVWVTSNFMVCVAMAATALISFWSLRDY 411
 VR GAFGLLLNSV LG SSFLIEPMC++G R+VW SNF+V MA TA+IS S+ +Y

Sbjct: 423 VREGAFGLLLNSVDLGISSFLIEPMCQRMGARLVWAMSNFIVFACMAGTAAISLVSNEY 482

Query: 412 HGY-VQDAITANASIKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLN 470
 +Q AI N +IK LV+FA LG PL+I YSVPF++TA+L A GGGQGL GVLN

Sbjct: 483 ITEGIQHAIGENRAIKIASLVVFALLGFPLSITYSVPFSITAELTADTGGGQGLAIGVLN 542

Query: 471 ISIVIPQVIIALGAGPWDALFGKGNIP 497
 ++IVIPQ+I++LGAGPWDALFG GNIP

Sbjct: 543 LAIVIPQMIIVSLGAGPWDALFGGGNIP 569

>gi|29467456|dbj|BAC67165.1| sucrose transporter [Oryza sativa (japonica cultivar)
 Length = 535

Score = 502 bits (1293), Expect = e-141

Identities = 261/489 (53%), Positives = 333/489 (68%), Gaps = 8/489 (1%)



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RPS-BLAST 2.2.5 [Nov-16-2002]

Query= local sequence:
(533 letters)Database: cdd.v1.61
10,927 PSSMs; 2,688,589 total columns

Click on boxes for multiple alignments

 Show Domain Relatives

PSSMs producing significant alignments:

Score E
(bits) valuegnl|CDD|11918 COG2211, MelB, Na+/melibiose symporter and related transporter... 47.9 3e-06

gnl|CDD|11918, COG2211, MelB, Na+/melibiose symporter and related transporters [Carbohydrate transport and metabolism]CD-Length = 467 residues, only 26.3% aligned
Score = 47.9 bits (114), Expect = 3e-06

Query:	42	PISLGRLILAGM--VAGGVQYGVWALQLSLLTPVQTLGLSHALTSMWLCGPIAGLVVQP	99
Sbjct:	8	KLSLKEKIGYGLGDFASNFAFG-IVVLYLLFFYTDVFGLSAALAGTIFLVAIIDAITDP	66
Query:	100	LVGLYSDRCTSRWGRRRPFILTGCMLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWH	159
Sbjct:	67	IMGFIVDRTRSRWGRFRPWLLWGAIPFAIVAVLLFITPDFS-----MTGKLIY	114
Query:	160	AAIVYVLGFWLDFSN	175
Sbjct:	115	ALVTYMLLGLGYTLVN	130

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RPS-BLAST 2.2.5 [Nov-16-2002]

Query= local sequence:
(533 letters)Database: cdd.v1.61
10,927 PSSMs; 2,688,589 total columns

Click on boxes for multiple alignments

 Show Domain Relatives

PSSMs producing significant alignments:

Score E
(bits) valuegnl|CDD|11918 COG2211, MelB, Na+/melibiose symporter and related transporter... 47.9 3e-06

gnl|CDD|11918, COG2211, MelB, Na+/melibiose symporter and related transporters [Carbohydrate transport and metabolism]

CD-Length = 467 residues, only 26.3% aligned
Score = 47.9 bits (114), Expect = 3e-06

Query:	42	PISLGRLILAGM--VAGGVQYGWALQLSLLTPYVQTLGLSHALTSMWLCGPIAGLVVQP	99
Sbjct:	8	KLSLKEKIGYGLGDFASNFAFG-IVVLYLLFFYTDVFGLSAALAGTIIFLVAIIADAITDP	66
Query:	100	LVGLYSDRCTS RWGRRRP FILTGCM LICVA VIVVG FSSD IGA ALGDT KEHCS L YHG PRWH	159
Sbjct:	67	IMGFIVDRTRSRWGRFRPWLLWGAIPFAIVAVLLFITPDFS-----MTGKLIY	114
Query:	160	AAIVYVLGFWLLDFSN	175
Sbjct:	115	ALVTYMLLGLGYTLVN	130

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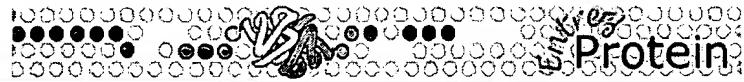
S Protein

PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books
Search	Protein	<input type="button" value="▼"/>	for				<input type="button" value="Go"/>	<input type="button" value="Clear"/>
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1: AAF90181. sucrose transport...[gi:9624451]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAF90181 538 aa linear PLN 07-APR-2003
DEFINITION sucrose transporter [Oryza sativa (indica cultivar-group)].
ACCESSION AAF90181
VERSION AAF90181.1 GI:9624451
DBSOURCE accession AF280050.1
KEYWORDS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (residues 1 to 538)
AUTHORS Aoki,N., Hirose,T., Scofield,G.N., Whitfeld,P.R. and Furbank,R.T.
TITLE The sucrose transporter gene family in rice
JOURNAL Plant Cell Physiol. 44 (3), 223-232 (2003)
MEDLINE 22555500
PUBMED 12668768
REFERENCE 2 (residues 1 to 538)
AUTHORS Whitfeld,P.R. and Furbank,R.T.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-2000) CSIRO Plant Industry, GPO Box 1600,
Canberra, ACT 2601, Australia
COMMENT Method: conceptual translation supplied by author.
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source Location/Qualifiers
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/cultivar="IR36"
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1..538
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CDS
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/coded_by="join(AF280050.1:1481..1717,
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AF280050.1:5208..5241,AF280050.1:5408..5507,
AF280050.1:5674..5749,AF280050.1:5975..6169,
AF280050.1:6288..6431,AF280050.1:6541..6774,
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AF280050.1:7184..7357)"
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1 margsgaggg ggggggggle1 svvgggggga rgggggeaaa avetaapisl grlilsgmva
61 ggvqygwalq lsltppvqt lglshaltsf mwlcgpiagm vvqpcvglys drctskwgrr
121 rpyiltgcvl iclavvvigf sadigyamgd tkedcsvyhg srwhaaivvv lgfwlldfsn
181 ntvqgparal madlsgrhgp gtansifcsw mamgnilgys sgstnnwhkw fpflktracc
241 eacanlkgaf lvavifslc lvitlifake vpfkgnaalp tksnepaepe gtgplavlkg
301 frnlptgmgs vlivtgtwl swfpfilydt dwmGREIYHG dpkgtdpqie afnqgvragna
361 fglllnsivil gfssfliepm crkvgprvvw vtsnflvcia maatalisfw slkdfhgvtq
421 kaitadksik avclvlfaf1 gvplavlysv pfavtaqlaa trggggqgct gvlnisivip
481 qvvialgaggp wdelfgkgni pafglasgfa liggvagifl lpkiskrqrfr svsmgggh



Protein

PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books	
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Display		default	<input type="button" value="▼"/>	Show: 20	<input type="button" value="▼"/>	Send to	File	<input type="button" value="▼"/>	Get Subsequence

□1: AAF90181. sucrose transporter...[gi:9624451]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAF90181 538 aa linear PLN 07-APR-2003
DEFINITION sucrose transporter [Oryza sativa (indica cultivar-group)].
ACCESSION AAF90181
VERSION AAF90181.1 GI:9624451
DBSOURCE accession [AF280050.1](#)
KEYWORDS
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (residues 1 to 538)
AUTHORS Aoki,N., Hirose,T., Scofield,G.N., Whitfeld,P.R. and Furbank,R.T.
TITLE The sucrose transporter gene family in rice
JOURNAL Plant Cell Physiol. 44 (3), 223-232 (2003)
MEDLINE 22555500
PUBMED 12668768
REFERENCE 2 (residues 1 to 538)
AUTHORS Whitfeld,P.R. and Furbank,R.T.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-2000) CSIRO Plant Industry, GPO Box 1600,
Canberra, ACT 2601, Australia
COMMENT Method: conceptual translation supplied by author.
FEATURES Location/Qualifiers
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/sub_species="indica"
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Protein 1..538
/product="sucrose transporter"
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CDS 1..538
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AF280050.1:4321..4386,AF280050.1:4719..4817,
AF280050.1:4906..4970,AF280050.1:5036..5120,
AF280050.1:5208..5241,AF280050.1:5408..5507,
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ORIGIN

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61 ggvqygwalq lslltpyvqt lglshaltsf mwlcgpiagm vvqpcvglys drctskwgrr
121 rpyiltgcvl iclavvvigf sadigayamgd tkedcsvyhg srwhaaivvv lgfwlldfsn
181 ntvqgparal madlsgrhgp gtansifcsw mamgnilgys sgstnnwhkw fpflktracc
241 eacanlkgaf lvaviflslc lvitlifake vpfkgnaalp tksnepaepe gtgplavlkg
301 frnlptgmmps vlivtgtlwl swfpfilydt dwmgreiyhg dpkgtdpqie afnqgvraga
361 fglllnsivil gfssfliepm crkvgrvww vtsnflvcia maatalisfw slkdfhgtvq
421 kaitadksik avclvlfafl gvplavlysv pfavtaqlaa trggggqlct gvnisisivip
481 qvvialgaggp wdeIfgkgni pafglasgfa liggvagifl lpkiskrqfr svsmgggh

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Protein

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□1: BAA83501. Sucrose Transporter [gi:5771354]

BLink, Domains, Links

LOCUS BAA83501 521 aa linear PLN 26-AUG-1999
DEFINITION Sucrose Transporter [Zea mays].
ACCESSION BAA83501
VERSION BAA83501.1 GI:5771354
DBSOURCE accession AB008464.1
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (sites)
AUTHORS Aoki,N., Hirose,T., Takahashi,S., Ono,K., Ishimaru,K. and Ohsugi,R.
TITLE Molecular cloning and expression analysis of a gene for a sucrose
transporter in maize (Zea mays L.)
JOURNAL Plant Cell Physiol. (1999) In press
REFERENCE 2 (residues 1 to 521)
AUTHORS Aoki,N.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-1997) Naohiro Aoki, Japan International Research
Center for Agricultural Sciences, Biological Resources Division;
1-2 Ohwashi, Tsukuba, Ibaraki 305, Japan
(E-mail:naoki@ss.jircas.affrc.go.jp, Tel:81-0298-38-6305,
Fax:81-0298-38-6650)
FEATURES Location/Qualifiers
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/organism="Zea mays"
/db_xref="taxon:4577"
Protein 1..521
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CDS 1..521
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61 yvqtlglsha ltsfmwlcp iaglvqvplv glysdrctar wgrrrpfil gcmliclavi
121 vvgfssdig a algdtkehcs lyhgprwhaa ivyvlgfll dfsnntvqgp arammadlcg
181 hhgpsaansi fcswmalgni lgyssgstnn whkwfpflit nacceacanl kgafolvavvf
241 lvmcltvtf fanevpvrgn qnlptkange vetepsgpla vlkgfknlpt gmpsvllvtg
301 ltwlswfpfi lydtdwmgre iyhgdpkgsn aqisafdegv rvgsgfl1ln sivlgfssfl
361 iepmcrkvgp rvvwvtsnfm vcvamaatal isfwslkdhy gyvqdaitas tsikavclvl
421 faflgvplai lysvpfavta glaatkgggq glctgvlnis ivipqviial gagpwdalfg
481 kgnipafgva sgfaliggvv gvfl1pkisk rqfravsagg h
//

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